Application No. 60/427,903, filed November 20, 2002 (the "'903 Application"). The~~, the~~ entire disclosures of these applications are ~~which~~ incorporated herein by reference. This application claims priority from the International Application pursuant to 35 U.S.C. § 365, and from the '903 Application pursuant to 35 U.S.C. §§ 119(e) and 365.--.

IN THE CLAIMS:

Please cancel claims 2-40, 56-82 and 84-122, without prejudice. In addition, please amend claims 1, 41-43, 45, 48, 51, 52, 54, 55 and 83 as provided below in the associated claim listing:

1. (Currently Amended) A process for producing at least one ~~haplotyped~~ genome wide map, comprising the steps of:

(a) preparing chromosome maps associated with at least one chromosome; and

(b) producing a portion of the at least one ~~haplotyped~~ genome wide map based on the chromosome maps, wherein the at least one genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

Claims 2-40 (Canceled).

41. (Currently Amended) A software arrangement which, when executed on a processing device, configures the processing device to produce at least one ~~haplotyped~~ genome wide map the software arrangement comprising ~~the steps of~~:

(a) a first set of instructions which are capable of configuring the processing arrangement to prepare~~preparing~~ chromosome maps associated with at least one chromosome; and

(b) a first set of instructions which are capable of configuring the processing arrangement to produce~~producing~~ a portion of the at least one ~~haplotyped~~ genome wide map based on the chromosome maps, wherein the at least one genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

42. (Currently Amended) The software arrangement according to claim 41, wherein the portion of at least one ~~haplotyped~~ genome wide map comprises at least one restriction site.

43. (Currently Amended) The software arrangement according to claim 41, wherein less than all subparts of the ~~haplotyped~~ genome wide map are produced in step (b) as ordered or unordered sets of contigs.

44. (Original) The software arrangement according to claim 41, wherein the chromosome maps are based on at least one single molecule map data set.

45. (Currently Amended) The software arrangement according to claim 41, wherein the ~~haplotyped~~ genome wide map comprises two maps per chromosome is assembled from the at least one single molecule map data set

46. (Original) The software arrangement according to claim 44, wherein the at least one single molecule map data set has error rates as great as or smaller than: about 10% error in distance between sites, about 20% missing sites, about 7% false sites and about 50% of sites closer than about 1 kB apart that are indistinguishable.

47. (Original) The software arrangement according to claim 44, wherein the at least one single molecule map data set consists of either Optical Mapping data or any single

molecule ordered maps of polymorphic markers comprising at least one of restriction site polymorphisms, restriction length polymorphisms, insertions of bases, deletions of bases, single nucleotide polymorphisms (SNPs).

48. (Currently Amended) The software arrangement according to claim 44, wherein the at least one single molecule map data sets comprising different restriction site markers are assembled into a single ~~haplotyped~~ genome wide map wherein all restriction site markers are combined and wherein the restriction site markers can be distinguished.

49. (Original) The software arrangement according to claim 41, further comprising determining a conditional probability density expression.

50. (Original) The software arrangement according to claim 49, wherein the probability density expression is based on errors provided in at least one single molecule map data set.

51. (Currently Amended) The software arrangement according to claim 41, wherein substantially all site based polymorphisms are detected in the at least one ~~haplotyped~~ genome wide map.

52. (Currently Amended) The software arrangement according to claim 41, wherein substantially all interval-based polymorphisms are detected in the at least one ~~haplotyped~~ genome wide map.

53. (Original) The software arrangement according to claim 41, wherein steps (a) and (b) are performed within a particular time limit, and the particular time is a sub-quadratic function of a number of sites associated with an input data.

54. (Currently Amended) The software arrangement according to claim 41, further comprising performing a disease gene association study based on at least one ~~haplotyped~~ genome wide map per patient.

55. (Currently Amended) A software arrangement which, when executed on a processing device, configures the processing device to perform disease gene association based on at least one haplotyped genome wide map per patient, the software arrangement comprising ~~the steps of~~:

(a) a first set of instructions which are capable of configuring the processing arrangement to generate~~producing~~ at least one haplotyped genome wide map per patient ; and

(b) a second set of instructions which are capable of configuring the processing arrangement to perform~~performing~~ the disease gene association based on the produced at least one haplotyped genome wide map.

Claims 56-82 (Canceled).

83. (Currently Amended) A system for producing at least one ~~haplotyped~~ genome wide map comprising a storage medium, wherein the storage medium includes software that is executed to perform the steps of:

(a) preparing chromosome maps associated with at least one chromosome; and

(b) producing a portion of the at least one ~~haplotyped~~ genome wide map based on the chromosome maps, wherein the at least one genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

Claims 84-122 (Canceled).